

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2003, 15:29:20 ; Search time 3325 Seconds
(without alignments)
5533.380 Million cell updates/sec

Title: US-09-494-297-2
Perfect score: 3945
Sequence: 1 MKKTRPNNKINTNTORVLS.....IAGISLGWGHITIRIKHD 757

Scoring table:
BLOSOM62
Xgapop 10.0, Ygapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlp
-O=/cgn2.1/USPTO.spool/US09494297/runat_13082003_122947_28105/app-query.fasta.1.903
-DB=EST -QFMT=fastcap -SUFFIX=first -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=-1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09494297.ecgn.1_1_2743-ctunat.13082003_122947_28105 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOBVERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=130 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	3.2	3344	11 BC028681	BC028681 Homo sapi
2	123.5	3.1	3778	11 AK079441	AK079441 Mus muscu
3	121	3.1	3617	11 AK084780	AK084780 Mus muscu
4	120	3.0	2138	11 AK031936	AK031936 Mus muscu
5	120	3.0	3959	11 AK031071	AK031071 Mus muscu
6	118.5	3.0	4594	11 AK036592	AK036592 Mus muscu
7	116	2.9	704	12 BM169720	BM169720 EST572243
8	115.5	2.9	708	12 BM674993	BM674993 UI-E-E30-
9	114.5	2.9	863	28 A2681177	A2681177 ENTMRA5TR
10	112.5	2.9	945	13 BX350683	BX350683 BX350683
11	112	2.8	2421	11 BC008707	BC008707 Homo sapi
12	112	2.8	2430	11 BC015953	BC015953 Homo sapi
13	111.5	2.8	1493	11 AK076636	AK076636 Mus muscu
14	111.5	2.8	2167	11 AK077916	AK077916 Mus muscu
15	111	2.8	889	28 BH132924	BH132924 ENTMX37TF
16	111	2.8	3250	11 BC047878	BC047878 Homo sapi
17	110	2.8	2419	11 AK035141	AK035141 Mus muscu
18	109	2.8	2673	11 BC040379	BC040379 Homo sapi
19	109	2.8	2677	11 AK016632	AK016632 Mus muscu
20	109	2.8	3044	11 AK042358	AK042358 Mus muscu
21	109	2.8	3318	11 AK032570	AK032570 Mus muscu
22	109	2.8	3493	11 AK080043	AK080043 Mus muscu
23	108.5	2.8	1085	12 BM913991	BM913991 AGENCOURT
24	108	2.7	626	10 BE919552	BE919552 EST423321
25	108	2.7	961	13 BX461833	BX461833 BX461833
26	107.5	2.7	584	9 AV603854	AV603854 AV603854
27	107.5	2.7	874	14 CD302015	CD302015 AGENCOURT
28	106.5	2.7	1320	11 AK016441	AK016441 Mus muscu
29	106.5	2.7	2955	11 AK089817	AK089817 Mus muscu
30	106.5	2.7	4415	11 AK076369	AK076369 Mus muscu
31	106	2.7	964	13 BX350916	BX350916 BX350916
32	106	2.7	3046	11 AK046668	AK046668 Mus muscu
33	106	2.7	3640	11 AK082842	AK082842 Mus muscu
34	105.5	2.7	596	13 BO591910	BO591910 E012582-0
35	105.5	2.7	783	10 BG681779	BG681779 602629706
36	105.5	2.7	1557	28 BH770729	BH770729 LMGtag47
37	105.5	2.7	1743	11 AY067850	AY067850 Schmidtea
38	105	2.7	961	29 CNS06VHB	AL417141 T3 end of
39	105	2.7	2880	28 BH770980	BH770980 LMGtag70
40	105	2.7	3416	11 AK041657	AK041657 Mus muscu
41	104.5	2.6	686	13 BM211560	BM211560 BM211560
42	104.5	2.6	741	13 BM212561	BM212561 BM212561
43	104.5	2.6	748	13 BM209345	BM209345 BM209345
44	104.5	2.6	2595	11 AK042706	AK042706 Mus muscu
45	104.5	2.6	2613	11 AK028919	AK028919 Mus muscu

ALIGNMENTS

RESULT 1
LOCUS BC028681 3344 bp mRNA linear HTC 01-MAY-2002
DEFINITION Homo sapiens, retinoic acid induced 14, clone IMAGE:4822221, mRNA.
ACCESSION BC028681
VERSION BC028681.1 GI:20379528
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 3344)
AUTHORS Strausberg, R.

TITLE Direct Submission
JOURNAL Submitted (29-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amandensystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 33 Row: c Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 13470085
This clone has the following problem: frame shifted.

FEATURES
source
1. .3344
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="locusid:26064"
/db_xref="taxon:9606"
/clone="IMAGE:482221"
/tissue_type="Testis"
/clone_id="NH_MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"

BASE COUNT 1170 a 691 c 782 g 701 t
ORIGIN

Alignment Scores:

Pred. No.: 0.0252 Length: 3344
Score: 128.00 Matches: 151
Percent Similarity: 35.72% Conservative: 98
Best Local Similarity: 21.66% Mismatches: 254
Query Match: 3.24% Indels: 195
Gaps: 36

US-09-494-297-2 (1-757) x BC028681 (1-3344)

QY 124 LysLysTrp--TyrLysLysHisAspGlyIleSerThrLysPheGluAspTyr----- 140
DB 1156 AAGAAGTGCMACTCCAAAAAGCAAGCTCCACACCTCATGCTGCTACCCAGTT 1215
QY 141 -----AlaMet-SerProArg---IleThrGlyAspGluLeuAsnGlnLysLeuArgAl 157
DB 1216 GAGTGAATGCTCTCCCAAGACATCACTGACTCCACTATCGGGAAG---GAATC 1272
QY 157 aValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLe 177
DB 1273 GGTATTTTTCGCAACCACTTCAGAGCTGAG-----AT 1308
QY 177 uAsnAlaIleArgValThrGlnGluAlaValTyrTyrSerAspAsnAlaProIleSe 197
DB 1309 CAGTTCTATACGAGAAACAAAGACAGACTA-----AGTACAGTACT-----AC 1353
QY 197 rAsnProAspGluSerPheLysArgGluSerGluSer-----AsnLeuValSerTh 214
DB 1354 AGGTGCTGATAGCTTATTTGATATTAAGTTCTGAAGCTGACCAACAAGATCTTCTCTCT 1413
QY 214 rSerGlnLeuSerLeuMetArgGlnAlaLeu-----LysGlnLeuIleAspProAsnLe 232
DB 1414 ATTGCAGCAAGCAAAAGTTGCTTCCCTTACCTTACCAATTAAGCACTTACCAAGAT---AAATT 1470
QY 232 uAlaThrLysMetProLysGlnValProAspAspPheGlnLeuSerIlePheGluSer-- 251

DB 1471 ACAGGCCAAATACACCAAGAGAGGGGAGCAGACAGCTTAAGCTTGACTCATACCATTCAC 1530
QY 252 ----GluAspLysGlyAspLysPheLysGlyTyrGlnAsnLeuSerGlyGlyLe 270
DB 1531 CCAAACTGACTGGGCCATCCCTCGGGA--- 1561
QY 270 uValProThrLysProThrProThrProGlyAspProPheProMetProProAsnGlnProGlnTh 290
DB 1562 -----CCTGGTGAA---ACCTTCGCCAGACTCCAAATCATC 1596
QY 290 rThrSerValIleuArgLysTyrAlaIleGlyAspTyrSerLysLeuLeuGluGlyAl 310
DB 1597 TCATCTGCTTATA-----CATCTTTAGG----- 1624
QY 310 aThrLeuGlnLeuThrGlyLysPheValAsnSerPheGlnAlaArgValPheSerSerAs 330
DB 1625 -----AAATCCACTACTGACATATGTCAGAAATTCACCACTGCAAGAGATTGCA 1677
QY 330 nAspIleGlyLysValIleGluLeuSerAsp----- 340
DB 1678 AGATCTACAGAGAGATTAGAGAGCTTGAGCAGAGAGAAACAGCTACAGTCCAGCT 1737
QY 341 -----GlyThrTyrThrLeuThrGluLeuAsnSe 350
DB 1738 CCAATCCGGAAGGCGACAGACTGATGCTTAACCAACACAGCATTTCAAGAAACAGCTC 1797
QY 350 rProAlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAlaGlyLysValTy 370
DB 1798 TGACCTCAGCAGCAAACTTAAAGAACTTAGACCAATACAGAGAGCTATGAAAGAGT 1857
QY 370 rThrIleIleAspGlyLysGlnIleGluAsnProAsnLysGluIleValGluProTyrSe 390
DB 1858 CCTTAGTGTCAG---AAGCAGATGAAA-----CTCGGCTTGCTCTCACCTGAAAG 1905
QY 390 rValGluAlaTyrAsnAspPheGluGluPheSerValLeuThrThrGlnAsnTyrAlaTy 410
DB 1906 CATGATATTAATTAATTCATTTCCACGAGCTGAGGCTCAGCAGAGAGAA---AATAATGTGC 1964
QY 410 sPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValValTyrCysPheAsnLys 430
DB 1965 T-----AAAGCAGATGCGAGA-----TGCAATTGAAAGAA 1997
QY 430 pLeuLysSerProProAspSerGluAsp---GlyGlyLysThrMetThrProAspPheTh 449
DB 1998 GTGAAGAATTAAGAAAGTACAGAGAGTACAGGAAACT----- 2040
QY 449 rThrGlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPheLysTyrThr--Val 469
DB 2041 -----GCTAGAGAGGAGAAAGTACAGTATTA 2069
QY 469 ySProArgAspThrAspProAspThrPheLeuLysHisIleLysLysValIleGlyLysG 489
DB 2070 AGCCACCTGTGAGAGAGTACGAGAAATGAAGAAATTCATATTCCTCTGTTATTTGAATA 2129
QY 489 lYrThrGluLysGlyGlnAlaIle-----GluTyrSerG 501
DB 2130 TGAATTAAGGAAAGCATTTTGTGTGAGAAATACCAAGAGCCCAAGAAATATCATGA 2189
QY 501 lYLeuThrGluThrGlnLeuArgAlaIleThrGlnLeuAlaIleTyrTyrPheThrAspS 521
DB 2190 AATTAAAGACACACTAAAGAGTCAGATGACACAGAGAGCC-----AGTGAAG 2237
QY 521 eAlaIa-----GluLeuAspLysAsp----- 527
DB 2238 AAGCTGAGACATGAAGAAGCCATGAATAGATGATAGATCAATTAACACAGCTGA 2297
QY 528 -----LysLeuLysAspTyrHisGlyPheG 536
DB 2298 GCGAGCTGTCACAGCTGTACAAAGAACCCAGGCTACAGCTGAGGATTTACAGAGAAAGGA 2357
QY 536 lYAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyr-----A 553

Db 2358 AATCTAGAGATGTACCA-----GCTGAATATATCCATAAG 2396
 Oy 553 laginaspserasrproptoglnteurhraspleu-----aspherp 567
 Db 2397 CAGGACATGAGAAACTGATGACAAACGCTCCAGGGCTAAAGCAGAAATGTCAC 2456
 Oy 567 helieproanasnlnstysrlnserleuilegltlthgltprhisplogluasp 587
 Db 2457 TGTCTGAATGAAGACTCAGATTCACAAAGTGTGAATGAGTACCCAGCTCAACAC 2516
 Oy 587 euvalaspilleleatgmetcluasplstysgluvalleprevalthrhisantaut 607
 Db 2517 TGTGGAT-----GCACAAAAGAGAACTGCTGTATCAGACAAATTTGC 2564
 Oy 607 hrleuaglysthrvalthrglyleuualaglyasparatgthrlsaspheisthegu 627
 Db 2565 AAGGATPACCCGCTG-----CGACATGCAGCAAAAGATGTGAAG 2606
 Oy 627 legluleuysasnlnsglngluleuSerGlnThrValsthrasplsthr 647
 Db 2607 AAAAATRACCAATCTTAAGGACACCTTGCACCAAGAGAGAGTGAAGTACCAAGCTG 2666
 Oy 647 snleuglupheylsaspelylsalathrlleasnleuylslygluSerleuthrl 667
 Db 2667 AGAACAACCTTGAAGAGAAAGCT-----CCTATGACTG 2702
 Oy 667 euglnglyleupro---GluGlytyrserlyrleuValsthrasplsthr 686
 Db 2703 ATGCAATGTACCTCGCTTCCTTCATAAAACCTCCATCCTTACAGAGTAA---- 2758
 Oy 686 ylrlsValsthrasplsthrGlnGluValsthrValsthrasplsthr 706
 Db 2759 -----GTGAGTGTCTTGCGATCGAATTAAGATCTGTCAAGAGAGAGAGGCTC 2813
 Oy 706 hrserasp-----gluthrlleualaphgluasnasnlysgluprov 720
 Db 2814 ATTCAGAGGTGTTCACATTAAGAGTGAAGTGTCAAGAGTGAAGAGAGAGAAATA 2873
 Oy 720 al-----ValProthGlyValaspGlnlyllesnnglyTYrleu 733
 Db 2874 TTCAGACTCTCTTGAATCCAAAGAGCAGAAAGTAATGAATCTCTG 2920
 RESULT 2
 AK079441 3778 bp mRNA linear HTC 05-DEC-2002
 LOCUS DEFINITION Mus musculus adult female vagina cDNA, RIKEN full-length enriched library, clone:9930026E20 product:desmocoilin 1, full insert sequence.
 ACCESSION AK079441
 VERSION AK079441.1 GI:26098508
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Carninci,P. and Hayashizaki,Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagasaka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,T., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 JOURNAL 20530913
 MEDLINE 11076861
 PUBMED
 REFERENCE
 AUTHORS
 4
 Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Aikawa,T., Hara,A., Fukunishi,Y., Kono,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gotohori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nkaido,I., Pesole,G., Quackenbush,J., Schmitt,L.M., Staudill,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletchner,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whitehead,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohsaki,S. and Hayashizaki,Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
 JOURNAL 21085660
 MEDLINE 11217851
 PUBMED
 REFERENCE
 AUTHORS
 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 JOURNAL 6 (bases 1 to 3778)
 REFERENCE
 AUTHORS
 Adachi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,M., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,M., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Kono,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahata,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
 Direct Submission
 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Chemical Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/.
 Location/Qualifiers
 1..3778
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"

FEATURES
SOURCE

COMMENT

TITLE
JOURNAL

REFERENCE
AUTHORS

TITLE

REFERENCE
AUTHORS

TITLE
JOURNAL
MEDLINE
PUBMED

REFERENCE
AUTHORS

JOURNAL
MEDLINE
PUBMED

TITLE

JOURNAL
MEDLINE
PUBMED

REFERENCE
AUTHORS

JOURNAL
MEDLINE
PUBMED

REFERENCE
AUTHORS

JOURNAL
MEDLINE
PUBMED

```

/db_xref="FANTOM_DB:9930026E20"
/db_xref="taxon:10090"
/clone="9930026E20"
/sex="female"
/tissue_type="vagina"
/clone_lib="RIKEN Full-length enriched mouse cDNA library"
/dev_stage="adult"
1.3778
misc_feature
/note="desmocolin 1 (MGD|MG:109173, GB|NM_013504,
evidence: BLASTN, 98%, match=2955)"
BASE COUNT    1148 a    829 c    811 g    989 t    1 others
ORIGIN

Alignment Scores:
Pred. No.:      0.0971      Length:      3778
Score:          123.50      Matches:     144
Percent Similarity: 31.62%      Conservative: 90
Best Local Similarity: 19.46%      Mismatches:  263
Query Match:      3.13%      Indels:      243
DB:               11      Gaps:         36

US-09-494-297-2 (1-757) x AK079441 (1-3778)
QY      102  ArgSerTyrGlnValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAsp--- 120
      |||||  :::::|||||  |||||  |||  |||||  |||
Db      532  AGAAGCTAGAAAGTGTACTGTGACGAAGAAAAAAGGTTT---TTAGCAAAAGACATA 588
QY      121  -----SerSerValLysLysTyrTyrLysLysHisAspGlyLe 133
      ::|||  :::::||||  |||||  |||||  |||
Db      589  CCAAGAGCCAGACAGCAACCGCCAGTAAAGAGAGTGGCTCT-----ATT 636
QY      134  SerThrLysPheGlnAspTyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGln 153
      ::  :::::||||  |||  :::::||||
Db      637  CCATGTTCACTGATGAGAACTCTTGGGTCCA----- 669
QY      154  LysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGlyGly 173
      |||||  ::|||  ::|||  ::|||  ::|||
Db      670  -----TTTCCACAACATTCAGATTCAGACAGCAATCTGAT 702
QY      174  LeuGluProLeuAsnAlaIleArgValThrGlnGluAlaValIleTyrTyrSerAspAsn 193
      |||  |||  |||  |||  |||  |||  |||  ::|||  |||
Db      703  -----GCTGCCAGAAATTACACCACTCTTATCTATACAGT 738
QY      194  AlaPro-----IleSerAsnProAspGluSerPheLysArgGluSerGluSerAsnLeu 211
      |||  |||  |||  |||  |||  |||  |||  ::|||  |||
Db      739  GGACGAGAGTAGACCAAGCCCTTACAAATTTGTTCTACATAGAAAGACCGGGGAC 798
QY      212  ValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsn 231
      :::::  :::::||||  |||||  |||  :::::
Db      799  ATCTATTGTACCCGA--AGCATTTGACCGTGAACAGTATGACCAATTTTGGTATATGA 855
QY      232  LeuAlaThrLysMetProLysGlnValProAspAspPheGlnLeuSerIlePheGluSer 251
      |||||  |||||  |||||  |||||  |||||  |||||
Db      856  TATGCAACAACATCTGATGCTATGCCCAAGACTACCTCTCCCTGCTGTTTAAGCTT 915
QY      252  GluAspLysGlyAspLysTyrAsnLysGlyTyr----- 262
      |||||  |||  |||  |||  |||  |||  |||
Db      916  GAAGATGACAATGAC-----AATGCCCATATTTTGAACCAAAATTAACAGTTTACT 969
QY      263  -----GlnAsnLeuLeuSerGlyLysLeuValProThrLysProProThrProGlyAsp 280
      :::::  ::|||  |||||  |||  |||  |||
Db      970  GTGCCGAAAAAATTGCCGATCTGGAACTTGCAAGTGGAAGTGCATAGACAAGAT 1029
QY      281  ProPro-----MetProProAsnGln 287
      |||  |||  |||  |||  |||  |||
Db      1030  GAGCCGAGAACTCTACACACTCGTGAAGTACAAAATCTTACACAAAATCCGACGAC 1089
QY      288  ProGlnThrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLeu 307
      |||  |||  ::|||  |||  ::|||  |||  ::|||
Db      1090  CCA-----AAGCACTTCTCATCACCACCAACACAGGTGTGATC 1128
QY      308  GluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPhe 327
      |||  |||  |||  |||  ::|||  |||

```

```

Db      1129  ACTACCAACACACACTTTTACTGACGAGAGAAATGTGACATTACAGCTA---GTGATG 1185
QY      328  SerSerAsnAspIleGlyGluArgIle-----GluLeuSerAspGlyThrThr----- 344
      |||  ::|||  |||  |||  |||  |||  |||
Db      1186  GAGGTACGAGACATGGGGGGCCAGCCCTTTGGTCTGTTACACCAAGGAACATACCATC 1245
QY      345  ---LeuThrGlnLeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPheLys 363
      |||  ::|||  |||  ::|||  |||  |||
Db      1246  TCACGTGAGAGATGAGATGACAACTGCGCATCTACCCCAAACTTTATCTACAGAA 1305
QY      364  ValGluAlaGlyLys----- 368
      |||||  ::|
Db      1306  GTAGAAGAAAAACGAATTGATGTGAGATTCTGAGATGCTGTCACAGCAAGATTGG 1365
QY      369  -----ValTyrThrIleIleAspGlyLysGlnIleGluAsn 380
      |||||  |||||  |||||  |||||  |||||  |||||
Db      1366  CCCAACACCCCTCCACTCGAAGGGGGTATATACATCTTAAGGGGAACGAAAGGAAAC 1425
QY      381  -----ProAsnLysGlu-----IleValGluProTyr 389
      |||||  |||||
Db      1426  TTCAAATGACACAGGATCCAAATACAAATGAAGGGGCTTGTGTGTGTCAGACCACTG 1485
QY      390  SerValGluAlaTyrAsnAspPheGlu---GluPheSerValLeuThrGlnAsnTyr 408
      ::|||  |||  ::|||  |||||  |||
Db      1486  AACTATGAAAGTACGCCCGCAAGTCACTGCAAAATTTGGTCTCT-----AATGAA 1536
QY      409  AlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValValTyrCysPheAsn 428
      |||||  |||  |||  |||  |||
Db      1537  GCCCACTTCACTAGCCTGCAACGCAACCAACCAATGTGCACCACTGCACT 1596
QY      429  AlaAspLysSerProProAspSerGluAspGlyLysLysThrMetThrProAspPhe 448
      ::|||  ::|||  |||  |||
Db      1597  GTGAAATTTAAA-----GACAGAGATGAGAGGCGCTGAGTGCACGACCAAGTGC 1644
QY      449  ThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPheLysTyrThrVal 468
      |||||  |||  |||  |||||  |||||  |||||
Db      1645  AAAGTATTCAGAGCAAGATGATGCTCCAGCGGCAAGAGCTCTCTGGGCTAC----- 1698
QY      469  LysProArgAspThrAspProAspThrPheLeuLysHisIleLysLysValIleGluLys 488
      ::  |||||  |||||
Db      1699  -----AAAGCGGTGAGCCCAAGACA----- 1719
QY      489  GlyTyrArgGluLysGlnAlaIleGluTyrSerGlyLeuThrGlnLeuArg 508
      |||||  ::|||  |||
Db      1720  -----AGCAGTGTGAAGCTTAAGGTAT----- 1743
QY      509  AlaIleThrGlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLys 528
      |||||  |||||  |||||  |||||
Db      1744  -----GAGATG 1749
QY      529  LeuLysAspTyrThrHisGlyPheGlyAspMetAsnAspSerThr-----LeuAlaValAla 546
      |||  |||  ::|||  |||  |||
Db      1750  GTAGAGAGATGAGATATTTGTTGAGATTTAACAAATACACCGGACACTTGAGAACTG 1809
QY      547  LysIleLeuValGluTyrAlaGluAspSerAsnProProGlnLeuThrAspLeuAspPhe 566
      |||||  |||||  |||||
Db      1810  AAAGTACTGACAGAGAGTCAAG----- 1833
QY      567  PheIleProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGlnThrPheProGluAsp 586
      |||||  |||||  |||||  |||
Db      1834  TTTGTGAAAAAACCAACAGTACATATTTAGTAGTGCAGCAGATACACCTGGCCGATCT 1893
QY      587  LeuValAsp-----IleIleArgMetGluAspLysLysGluValIleProValThrHis 604
      ::|||  ::|||  |||||
Db      1894  TGCACAGGAACACTGCTAGTCTTCTGGAAGATTTTAATGAC-----CAC 1938
QY      605  AsnLeuThrLeuArgTyrThrValThrGlyLeuAlaGlyAspArgThrLysAspPhe--- 623
      ::|||  |||  |||||  |||
Db      1939  CCACGACAGATTGACAGAAGATGACC-----ATTGTGCAGAGAGAAAGATTTTGGT 1992
QY      624  -----HisPheGluIleGluLeu 629
      |||||  |||||
Db      1993  GTTTTGAACTATAGATTAGATGGGCGACAGATATAGTGCACCTTTTCAGTTCCCTTCG 2052

```

OY 630 LysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnGlu 649
 DB 2033 GATATTTCTTCACGCAAACTTGGACT-----CTAGAA 2085
 OY 650 PheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyGluSerLeuThrLeuGlnGly 669
 DB 2086 TCACAGCATGCTAAACGTCGCATCTCTGCTCAACACACACATCTTATAT----- 2136
 OY 670 LeuProGluGlyTyrSerTyrLeuValLysGlnThrAspSerGluGlyTyrLysValLys 689
 DB 2137 -----AACTATTATTTCTGTCGCATCCAAATACACAGACAGCATGTTTCCCAAAA 2190
 OY 690 ---ValAsnSerGlnGluValAlaAsnAlaThrValSerLysThrGlyIleThrSerAsp 708
 DB 2191 CATGATTATTCATCGACGAGTGTGACGTGCATCACT-----CCACACAGA 2235
 OY 709 GluThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyValAspGlnLys 728
 DB 2236 TGTGCAATGCGCTTTAAGCAAGACAGC-----GATGCTAAA 2271
 OY 729 IleAsnGlyTyrLeuAlaLeuIleValIleAlaGlyIleSerLeuGlyIleTrrpGlyIle 748
 DB 2272 CCAAAAT-----ATAATCCTTGGCAATGCGCAGCAT 2301
 RESULT 3
 AK084780 3617 bp mRNA linear HTC 05-DEC-2002
 LOCUS AK084780 Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched
 DEFINITION library, clone:D330041119 product:TRIN homolog [homo sapiens],
 full insert sequence.
 ACCESSION AK084780.1 GI:26351280
 VERSION AK084780.1
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M.,
 Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, T.,
 Yoneda, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
 Takeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 JOURNAL sequencing pipeline with 384 multicapillary sequencer
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Aizawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanka, I.,
 Saito, T., Okazaki, Y., Gojodori, T., Bono, H., Kasukawa, T., Saito, R.,
 Kado, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
 Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
 Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,

Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M.,
 Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
 Baldarelli, R., Barsh, G., Blake, J., Botelli, D., Bojunga, N.,
 Carninci, P., de Bonaldo, M.F., Brownstein, M.D., Bull, C.,
 Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
 Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
 Ring, B., Rungwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
 Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
 Toyo-oka, K., Wang, K.H., Weitz, C., Whitlaker, C., Wilming, L.,
 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohlsuk, S.
 and Hayashizaki, Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research
 JOURNAL Group Phase I & II Team.
 MEDLINE Analysis of the mouse transcriptome based on functional annotation
 PUBMED of 60,770 full-length cDNAs
 REFERENCE Nature 420, 563-573 (2002)
 TITLE 6 (bases 1 to 3617)
 JOURNAL Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P.,
 Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirakawa, T., Hirozane, T.,
 Hori, F., Imoto, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koyama, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shitaki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, E., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp,
 URL: http://genome-gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome-gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/.
 FEATURES
 source location/Qualifiers
 1. 3617
 /organism="Mus musculus"
 /mol_type="cDNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM:DB:D330041119"
 /db_xref="taxon:10090"
 /clone="D330041119"
 /tissue_type="heart"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="13 days embryo"
 <1. >3617
 /note="unnamed protein product; TRIN homolog [homo
 sapiens] (SPTRI/CAD12456, evidence: FASTY, 97.2&ID,
 3.5&length, match=3615)
 putative"
 /codon_start=3
 /protein_id="BAC39277.1"
 /db_xref="GI:26351281"
 /translation="NARCTGKRSRPSKPTVAMPDIPAPGKPNPRTVDTTSTSLAW
 SVPEEGSKVYGLIEIMOKVDQREMTGNTPTPIRETTLHLPGQAEYRRLVACN
 AGGPEPAFVETGVATVEMLEPDELDERVOEGFVAGGVIIRLTIRIKKPFVCK

LOCUS	AK031936	2138 bp	mRNA	linear	HTC 05-DEC-2002
DEFINITION	Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6350501K11 Product:phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55), full insert sequence.				
ACCESSION	AK031936				
VERSION	AK031936.1 GI:26082605				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 Carninci, P. and Hayashizaki, Y.				
AUTHORS	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubuchi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076661				
REFERENCE	4				
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, K., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanka, I., Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R., Kaotaka, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochava, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staahl, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamuya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombere, P., Nordone, P., Ring, B., Ringwald, C., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, J., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S. and Hayashizaki, Y.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409 (6821), 685-690 (2001)				
MEDLINE	21085660				
PUBMED	11217851				
REFERENCE	5				
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
JOURNAL	Nature 420, 563-573 (2002)				
MEDLINE	6 (bases 1 to 2138)				
PUBMED	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,				
REFERENCE	Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, R., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akhiba, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.				
ORGANISM	Direct Submission				
TITLE	Submitted (16-JUL-2001) Yoshinori Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Chemical Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suenitcho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)				
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers				
FEATURES	source				
misc_feature	1..2138				
polyA_signal	/organism="Mus musculus"				
polyA_site	/mol_type="mRNA"				
BASE COUNT	/strain="C57BL/6J"				
ORIGIN	/db_xref="FANTOM.DB:6350501K11"				
Alignment Scores:	/db_xref="taxon:10090"				
Pred. No.:	/clone="6350501K11"				
Score:	/sex="male"				
Percent Similarity:	/tissue_type="medulla oblongata"				
Best Local Similarity:	/clone_id="RIKEN full-length enriched mouse cDNA library"				
Query Match:	/dev_stage="adult"				
DB:	311..1697				
US-09-494-297-2 (1-757) x AK031936 (1-2138)					
271 ValProThylsProThrProGlyAsp-ProprometProProAsnGlnProGlnTh					
419 CTTCCACCAAGCCACCTAAGCCCAATGACCTCAGACATGCACAAATGCAACAGACAG					
290 r---ThrsValleuilearglystyralaileglyaspysrlyslleuileugluc1					
479 TTTCAATTCCTCTCAAGATGCACTGACGAGGACATATTCCAGG-----					
309 yalaThreuglnleuthrlygaspasvalasnsrheglnalaagvalpheserSe					
528 -----GAGAGGTAAATGACAAATTTGGGAGCATGCCAGATGCTTCTTACT					
329 rAsnspIlelglyguatrgilegluleuSeraspIlythrlyrrhrleuthr-----					
346					

Db 578 TCCTGATGCCCTCAGCAAAATGCGA-----GGGGATTATACATTGACTTTGAGGAA 628
 QY 347 -----GLeuAaSerProAlaGlyTyrSerIleAlaG1 358
 Db 629 GGGAGGAATTAATAATTATAAGATCTATCATCGGATGTAATATATGCTTCTCTGA 688
 QY 358 uProIleThrPhe----- 362
 Db 689 GCCCTGACGTTACTTCTGTGGTGGAGCTTATTACCACTACACACAGCTCTCTCGC 748
 QY 363 -----LysValGluAlaGlyLysValTyrThrIleAlaSerGlyLysGln-- 377
 Db 749 TCAGTACAAATCCCAACTCGACCTGAGCTGACGTCCAGATCCAGATTCACACAGGA 808
 QY 378 -----IleGluAsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrAs 395
 Db 809 TCAGTGTGTAAGAAGATTAACATGATGATGAGTAAATAATCTGCAGAGATTCACATC 868
 QY 395 nAspPheGluGluPheSerValLeuThrThrGlnAsnTyrAlaLysPheTyrAlaLys 415
 Db 869 TCAGTATCAGAGAAAGAGC-----AAAGATATGACAGCGCTGTAT-----GA 910
 QY 415 sAsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProPr 435
 Db 911 AGAGTACACAGAGCATCACAGAAATA----- 938
 QY 435 oAspSerGluAspGlyGlyLysThrMetThrProAspPheThrThrGlyValValLysTyr 455
 Db 939 -----CAAATGAAGAG 949
 QY 455 rThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspPr 475
 Db 950 GACTGCCATT-----GAACCTTTATATGAACAATTAATATTTGACAGAGCATG 1000
 QY 475 oAspThrPheLeuHisIleLysLysValIleGluLysGlyTyrArgGluLysGly 495
 Db 1001 TCATTACCAAGAACCAACAGTAACTATATCGAGCGC---TTTCGCGAAGAGGCGAA 1057
 QY 495 nAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaI 515
 Db 1058 TGAGAGAGAGATGCGACGAATATG----- 1082
 QY 515 eTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPh 535
 Db 1083 -----ATGATATTATGATTAATGCAATCA-----CGCTC 1111
 QY 535 eGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAs 555
 Db 1112 TGCTGAGATTCAATGATACCAACTGCGCTTGGAGCGAGCTTGAAGAACACACTTTGGA 1171
 QY 555 pSerAsnProProGluLeuThrAspLeuAspPheIleProAsnAsnAsnLysTyrG1 575
 Db 1172 CAACCGG-----GAATATAGAT-----AAAAAATGAA 1198
 QY 575 nSerIleuIleGlyThrGlnThrPheIleProGluAspLeuValAspIleIleArgMetGluAs 595
 Db 1199 TAGCAATC-----AAACCCGACTGATCCACTCGTGAAGATCCGGGA 1240
 QY 595 pLysLysGluValIleProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLe 615
 Db 1241 T---CAGCACTGTATGCTCAATACAGA----- 1268
 QY 615 uAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnG1 635
 Db 1269 ----GGAGTAGAGCAGACGGCGCTGAATGCTGCGGAGATCAAGAAATGAGACATCAGA 1324
 QY 635 uLeuLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPheLysAspGlyLysAl 655
 Db 1325 T---GAACCTATTATTATCAATGAGAGATGAGAACTGCGCCATTATGATGAGAAAC 1381
 QY 655 a-----ThrIleAsnLeuLysHisGlyLysGlnSerLeuThrLeuGlnGlyLeuPr 671
 Db 1382 CTGGTTTGGAGGATATACACCGAGTACACAGCAGAGACTTG---CTTATGGAACACC 1438

QY 671 oGluGlyTyrSerTyrLeuValLysGluThrAspSerGluGly---TyrLysValLysYa 690
 Db 1439 AGATGGT---GCATCTCTATTCTGTAGAGATACAGAAAGATGTTAGCTTGTCTGT 1495
 QY 690 lAsnSerGln---GluValAlaAsnAlaThrValSerLysThr 703
 Db 1496 GCTTGCAGACGGGGAAGTGAACGACCTGTCACTACAGCAGC 1538
 RESULT 5
 AK053071
 LOCUS
 DEFINITION
 AK053071 3959 bp mRNA linear HTC 05-DEC-2002
 Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
 library, clone:D930043C02 product:MEMBRANE-ASSOCIATED NUCLEIC ACID
 BINDING PROTEIN (FRAGMENT) homolog [Homo sapiens], full insert
 sequence.
 ACCESSION
 VERSION
 AK053071.1 GI:26095552
 KEYWORDS
 HTC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS
 Carninci, P. and Hayashizaki, Y.
 TITLE
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 JOURNAL
 MEDLINE
 PUBMED
 99279253
 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 JOURNAL
 MEDLINE
 PUBMED
 20499374
 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwake, S., Inoue, K., Togawa, Y., Ozawa, K., Tanaka, T., Matsura, S.,
 Yoneda, Y., Ishikawa, T., Inoue, Y., Kira, A. and Hayashizaki, Y.
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 JOURNAL
 MEDLINE
 PUBMED
 20530913
 11076861
 4
 Kawai, T., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, K.,
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
 Fleischmann, M., Gaasterland, T., Glisic, C., King, B., Kochiwa, H.,
 Kuehl, P., Lewis, S., Matsuo, Y., Nikidol, I., Pesole, G.,
 Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M.,
 Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
 Balderelli, R., Barsch, G., Blake, J., Boffelli, D., Bojunga, N.,
 Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
 Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
 Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, J., Mombauts, P., Nordone, P.,
 Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
 Sato, K., Schombach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,
 Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L.,
 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.
 and Hayashizaki, Y.
 TITLE
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
 JOURNAL
 MEDLINE
 PUBMED
 21085660

[illegible][illegible]

```

OY 344 -----ThrlleuThrgluLeuAsnSerProAlaGlyTyr----- 354
DB 2484 CCGAATGACCAAGCAAGCACTGTGCTTACCAAGGAACCTTGTGCTATTTGAAGACC 2543
OY 355 SerIleAlaGluProIleThrPheLysValGluAlaGlyLysValTyr----- 370
DB 2544 AGTTGGAGAACAGTAAAGAACAGCCAGATGACAGACAGATTCATACCCAGAAA 2603
OY 371 -----ThrlleleAspGlyLysGluIleGluAsnProAsnLysGluIle 385
DB 2604 AACACGTCTCTTCAACTCTCTGTGGCCACACAGTCCACACACCACTTCTCTCTA 2663
OY 386 ValGluProTyrSerValGluAlaTyrAsnAspPheGluIlePheSerValLeuThr 405
DB 2664 -----TTCACTAGACTTCGATCGATTCCTCTGAG-----AGT 2699
OY 406 GluAsnTyrAlaLysPhe-----TyrTyrAlaLysAsnLysAsnGly 419
DB 2700 GTGAGTGGCGCAAAATTTGAGAACACATCTTCCCATTTATCTCCGTGTGTGTGT 2759
OY 420 SerSerGluValValTyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAsp 439
DB 2760 ACC-----ATAGCTCTTGTATTAATGCCATGATTCGAGCCCAAGACGTAATGCT 2813
OY 440 GlyGlyLysThrThrProAspPheThrThyGlyLysValLys--TyrThrHisIle 458
DB 2814 AATTCAAAATGCTGTATGATGACCTGGACAGTGGGATGTAAAGAACAGTGCAT--- 2870
OY 459 AlaGlyArgAspPheLysTyrThrValLysProArgAspPheThrProAspThrPhe 478
DB 2871 -----TTATTGAAAGCTCAGAGAACGAAACAAAGAACAGCCCA----- 2909
OY 479 LeuLysHisIleLysValIleGluLysGlyTyrArgGluLysGluIleGlu 498
DB 2910 -----ATTATTCCTTACTAGACGAGCAACCATATTCACAAATGGGGTGAATTC 2960
OY 499 TyrSerGlyLeuThrGluThrGluLeuAlaAlaThrGluLeuAlaIleTyrPhe 518
DB 2961 CGATTCCTCCGCAAGAGT-----TACCATACA 2987
OY 519 ThrAspSerAlaGluLeuAspLysAspLys-----LeuLys 530
DB 2988 ACGATCCCGCTCCAGGCACTGCTCCCAAGAGATGCACTAACCCCATCAGCGTATCA 3047
OY 531 AspTyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuVal 550
DB 3048 GATTATGCTCCCTACGATGCTGTGCATTCAGTCAAGGAGAGT----- 3089
OY 551 GluTyrAlaGluAsp---SerAsnProProGluLeuThrAspLeuAspPheIlePro 569
DB 3090 TCATATGGCAACGATCTATCATCATCAGCACTATATTCGAACGGACGATTCATTTG 3149
OY 570 AsnAsnAsnLysTyrGlnSerLeuIleGlyThrGluThrPheProGlu-----AspLeu 587
DB 3150 ACTGAT-----TTATCTGTCATAGAAAGCATCTGATACCGAGACCTT 3194
OY 588 ValAspIleLeuArgMetGluAspLysGluValIleProValThrHisAsnLeuThr 607
DB 3195 TTGACGATTGAACCTTACAGAGCCAG-----AGTAACTATTACTT 3236
OY 608 LeuAlaGlyLysThrValThrGlyLeuAla-----GlyAspArgThrLysAsp 622
DB 3237 CTTTCACAGAGGAACCTAATGCTCTGCGCATTCACAAAGATGCAATTCCTCGATGAGGC 3296
OY 623 PheHisPhe-----GluIleGluLeuLysAsnAsnLysGluGlu 635
DB 3297 CGTCACCTTACTTTAAATCTTCTTAACCAAGAAATGAACTAAGAAATGAGAGAAATGAC 3356
OY 636 LeuLeuSerGluThrValLysThrAspLysThrAsnLeuGluPheLysAspGlyLysAla 655
DB 3357 TACACAGAGACACCTAGATACA---AAGCGCTGATAGGATATTTGAG----- 3401
OY 656 ThrIleAsnLeuLysHisGlyLysLeuThrLeuGluGlyLeu-----Pro 671

```

```

DB 3402 -----TTAGACTTTCACCCCTTGATCTAGTGAACCT 3434
OY 672 GluGlyTyrSerTyrLeuValLysGluThrAspSerGluGlyTyrLysValLysValAsn 691
DB 3435 GATGGCCAGAGTCAACAAATTTGAAGAAATTTGGACATACACCTGTGTACAGTTCTCA 3494
OY 692 SerGlnGluValAlaAsnAlaThrValSerLysTyrGlyIleThrSerAsp----- 708
DB 3495 AATGACCAAGTGTCTCAATGGAACAGCATGGAAGAAATGTCTCA-TCCAGCCAGACGACCA 3553
OY 709 -----GluThrLeuAlaPheGluLysAsnLysGluProValPro 722
DB 3554 GAAGGACCCAGAAAGCCGAAAGAGACAGATTTAGGAGGAGCGAACCAATTCGCG 3613
OY 723 ThrGlyVal-----AspGluLysIleAsnGlyTyrLeuAlaLeuIle 736
DB 3614 GTAACATCTTGTCTTAAAGCCAGCACGTCACATGCTATTATGACGTGCAAGTCCCTCCC 3673
OY 737 ValIleAlaGlyIleSerLeuGly-----IleTyrGlyIleHisThrIleArgIleArg 754
DB 3674 ATGACCAACATCTGTCACTGTGTGGCAACCTCATTTCTGAATTCGTTATGTGAAGAT 3733
OY 755 LysHisAsp 757
DB 3734 AAAAACGAC 3742

```

```

RESULT 6
LOCUS AK036592
DEFINITION Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:983013J03 product:transcription elongation factor B (Sirt), polypeptide 3 (110kd), full insert sequence.
ACCESSION AK036592
VERSION AK036592.1 GI:26331353
KEYWORDS HTC, CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1
  Carninci, P. and Hayashizaki, Y.
  High-efficiency full-length cDNA cloning
  Meth. Enzymol. 303, 19-44 (1999)
  99279253
  10349636
REFERENCE 2
  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
  Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
  Genome Res. 10 (10), 1617-1630 (2000)
  20499374
  11042159
REFERENCE AUTHORS
  Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, E., Watanabe, M., Takeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
  RIKEN integrated sequence analysis (RISA) system -384-format sequencing pipeline with 384 multicapillary sequencer
  Genome Res. 10 (11), 1757-1771 (2000)
  20530913
  11076861
REFERENCE MEDLINE
  4
  Kawak, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Iizawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, K., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,

```

Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Niesole, G., Ouekenbush, J., Schriml, L.M., Stanbly, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carinici, P., de Bonaldo, M.F., Brownstein, M.J., Bull, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamliya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S. and Hayashizaki, Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5

AUTHORS The FANTOM consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4594)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arawaka, T., Bono, H., Carinici, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawaji, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsumi, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehito-cho, Tsunumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES Please visit our web site for further details.

SOURCE URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers

FEATURES 1. 4594

SOURCE /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:9830138J03"
/db_xref="taxon:10090"
/clone="9830138J03"
/sex="male"
/tissue_type="bone"
/clone_id="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
26. 2347

CDS /note="unannotated protein product: putative transcription elongation factor b (STII), polypeptide 3 (110kd) (MGDI MG1.1351315, GB|NM_013736, evidence: BLASTN, 99%, match=2537)"
/codon_start=1
/protein_id="BAC29497.1"
/db_xref="GI:263131534"

/translation="MAESALQVEKIQARLANPDPKLLKLYIKLSTLPTVDILV
ETGEGTVNSRKRHEQGNFARDLVIAQKKVLPERNSEADDOPEKNSKRDRDL
ORRELEGNVOESMKPGSRVSYPENHKKKIKLSPPRPKVAHKKRREKCH
VSPYSDSPESDIGHVOSPSPSPHOMTDLSSPEDDPTTISHQPCGVHNTFO
RLDGVSHLEGQKCAVSHHKKRSHSKRKHADRADEKISAVREKSHKSKSESR
RILGVSHKEGKPSVYKDKDRSGSSKRPALDVAHNRKRPKDKSEKESR
KINSDVSGDGRSTYDQPKRKKVYKTSPTALGEGKLRKDSKSTKMLNSAOKL
DDEFRPMSPESTLYSDQPKRKKVYKTSPTALGEGKLRKDSKSTKMLNSAOKL
PKVNESEKIQAPGAEPTRRKVPDVLAPLPIPAIYANRPDPSLELISFOP
KRKAFSFEDEEAGFTGRNNSKMYTSGSKAYLRMMTLHOQKIRVKNIDSTF
EVGVPSVLEPERCTPDLYRIEENHVLIEETQDLKMHVCHHDKPEKPEYES
WRREYLRQDAREQRLRLTNNISGSSAHNKKRQAKMAFVNSVAKPPRDVRRQEF
GTGGAAYDEKVRKIPAPYTTSSHPVANSNSNFSPEELAYDGPSTSHALPVS
SSVSDPRKPAVKKIAIPMATIATFAKRFRR"

TITLE polyA_signal

JOURNAL /note="putative"

MEDLINE 4574. 4579

PUBMED /note="putative"

REFERENCE 4594

AUTHORS polyA_site

BASE COUNT 1278 a 1091 c 1108 g 1117 t

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Mismatches:	Best Local Similarity:	Query Match:	DB:
0.477	4594	118.50	100	59	148	35.25%	3.008	11
Percent Similarity:		35.25%						
Best Local Similarity:		32.17%						
Query Match:		3.008						
DB:		11						23

US-09-494-297-2 (1-757) x AK036592 (1-4594)

QY 99 GluGlySerArgSerTyrGlnValTyrCysPheAsnLeuLysAlaPhe----- 115

DB 923 GAAGGCACAC-----AGTCACAGAAAGAACTTTTCACCTGCC 958

QY 116 ---ProLeuGlySerAspSerSerValLysLysTyrLysLysHis---AspGlyLe 133

DB 959 TTACATGCTGCTTACAGACACCTTTAAAAAG-----CCCAACACACAGACTCCGAG 1012

QY 134 SerThrLysPheGlu-----AspTyrAlaMetSerProArgLleThr 147

DB 1013 AAAGCAAAATCTGACAAACAGACAGATGATGCGCGAGCTCAGACGAGGACA 1072

QY 148 GlyAspGluLeuAsnGlnLysLeuArgAlaValMetTyrAsnGlnHisProGln----- 165

DB 1073 GGAAGACCATTCGCCAAGAGAGAAAGTTCCCAACACCTGAAAGCTCAGAGGGG 1132

QY 166 -----AsnAlaAsnGlyTleMetGluGlyLeuGluProLeuAsnAla----- 179

DB 1133 AAAGTAGAAGTAAACGACGATGAGAAAGTACAGAGC-----CCGCTCCACCTTAAACG 1186

QY 180 -----11leArgValThrGlnGlnAlaValTyrPyr 190

DB 1187 GAGGAGACAGATGTGAGCAGATGATGTGAGCGGCCACGAGTGCCTTGCAGTCCACCTC 1246

QY 191 SerAspAsnAlaProIleSerAsnProAspGluSerPheLysArgGluSerGluSerAsn 210

DB 1247 AGCTATGACCAAGCC-----CGGAAGAAAGAAAGAGAG 1279

QY 211 LeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleAspPro 230

DB 1280 GTTGTGAAACGCTCCAGTACAGCAGCTTGGAACAAAAGACTTTAAAAAAGACTCTAA 1339

QY 231 -----AsnLeuAlaThrLysMetProLysGlnValProAspAspPhe 244

DB 1340 AGCAGTAGTAATAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1381

QY 245 GlnLeuSerIlePheGluSerGlnAspLysGlnLysLysLysGlyTyrGlnAsn 264

DB 1382 -----GTCACAGAAACAAAGACGACAGAG----- 1405

QY 265 LeuLeuSerGlyGlyLeuValProThrLysPro-----Pro 276

Db 1406 TTCACGACGACCTGGAGCCGGAACCCACAGGCTCGAAGGTCCTACTGATGTGTCACA 1465
 QY 277 ThpProGlyAspProPrometPro-----ProAsnGln 287
 Db 1466 GCATTGGCAGACATCCCTTACTCTGATTCATGACCACTACGGGCCCTTCCTCCCTT 1525.
 QY 288 ProGlnThpThpSerValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 307
 Db 1526 GAGTGTATTCCTCCCTTTCAGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 1576
 QY 308 GluGluValAlaThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 327
 Db 1577 GAAGAAGAAAGAACCTGGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1633
 QY 328 SerSerAsnAspIleGlyGlu-----Arg 335
 Db 1634 TCTGCTTCACAGTGTGCTATCTCCCAAAATGATGACATTCACACGACGATGATCCGG 1693
 QY 336 IleGluLeuSerAspGlyThpThpThpThpThpThpThpThpThpThpThpThpThpThp 355
 Db 1694 GTG---CTTAAAGATATATATGACTCTATCTTGAAGTAGAGAGA---GTCCCTATCTT 1747
 QY 356 IleAlaGluProIleThrPheLysValGluAlaGlyLysValThpThpThpThpThpThp 375
 Db 1748 GTTCTTGACCTGTCTTGAGAGAGGTCACACCTGATCAGCTCTAC-----1792
 QY 376 LysGlnIleGluAsnProAsnLysGluIleValGluPro-----TyrSerVal 391
 Db 1793 ---CGATATGAGAGATATGATCATGTATATATGAAAGAACACATGATGTGTGAAAGTT 1849
 QY 392 GluAlaTyrAsnAspPheGluGluPheSerValLeuThpThpThpThpThpThpThp 411
 Db 1850 CACTGTACCGAGCACTTAAAGAAAGAGCCAGAGAGATGATGCTGAGGAGATG 1909
 QY 412 Tyr-----412
 Db 1910 TACCTGAGGCTTCAGAGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1969
 QY 413 ---TyrAlaLysAsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAsp 430
 Db 1970 TCTGCTATCCCAATATAGCCAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2029
 QY 431 LeuLysSerProProAsp-SerGluAspGlyLysThpMetThpProAspPheThpThp 450
 Db 2030 GCCAAGCCCAACAGAGATGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2078
 QY 450 rglGluValLysTyrThpThpThpThpThpThpThpThpThpThpThpThpThpThp 460
 Db 2079 -GGGGAG 2108
 RESULT 7
 LOCUS BM169720 704 bp mRNA linear EST 04-DEC-2001
 DEFINITION EST572243 PyBS Plasmodium yoelii yoelii cDNA clone pYCPV60 5' end,
 mRNA sequence.
 ACCESSION BM169720 GI:17302952
 VERSION BM169720
 KEYWORDS EST.
 SOURCE Plasmodium yoelii yoelii
 ORGANISM Plasmodium yoelii yoelii
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 REFERENCE 1 (bases 1 to 704)
 AUTHORS Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Valdivia,A.B.,
 Fraser,C.M. and Garucci,D.J.
 TITLE Plasmodium yoelii EST project at TIGR
 JOURNAL Unpublished
 COMMENT Contact: Jane Carlton
 Parasite Genomics Group
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-530-9319
 Fax: 301-838-0208
 Email: carlton@tigr.org

For clone info, please contact the Malaria Research and Reference
 Reagent Resource Center, ATCC
<http://www.malaria.mf.org/mr4pages/index.html>
 Seq primer: ADP.
 FEATURES
 source
 Location/Qualifiers
 1..704
 /organism="Plasmodium yoelii yoelii"
 /mol_type="mRNA"
 /strain="17XL"
 /db_xref="taxon:73239"
 /clone="PYCPV60"
 /dev_stage="Asexual blood stages"
 /lab_host="E. coli XL-1 Blue"
 /note="Vector: PAD-GAL4: At 20-25% parasitemia, blood was collected from BALB/cBYJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (PAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."
 BASE COUNT 311 a 50 c 136 g 207 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.0464 Length: 704
 Score: 116.00 Matches: 54
 Percent Similarity: 38.70% Conservative: 47
 Best Local Similarity: 20.69% Mismatches: 86
 Query Match: 2.94% Indels: 74
 DB: 12 Gaps: 11
 US-09-494-297-2 (1-757) x BM169720 (1-704)
 QY 368 LysValTyrThpThpThpThpThpThpThpThpThpThpThpThpThpThpThpThpThp 387
 Db 57 AAAAAAAAAATTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 110
 QY 388 ProTyrSerValGluAlaTyrAsnAspPheGluGluPheSerValLeuThpThpThpThpThp 407
 Db 111 AGTTATATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 155
 QY 408 TyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValValTyrCysPhe 427
 Db 156 -----CCTGATGGGAGAGGCTGTCGAGAGATGATGATGATGATGATGATGATGAT 194
 QY 428 AsnAlaAspLeuLysSer-----ProProAsp 436
 Db 195 GAGCGACACATTTGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 254
 QY 437 SerGluAspGlyLysThpMetThpProAspPheThpThpThpThpThpThpThpThpThp 456
 Db 255 AGTGATATATGTCAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 314
 QY 457 HisIleAlaGlyArgAspLeuPheLysTyrThpValLysProArgAspThpAspProAsp 476
 Db 315 GATATA-----AAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 344
 QY 477 ThrPheLeuLysHisIleLysValIleGluLysGlyTyrArgGluLysGluAla 496
 Db 345 GATATATATATATATCTGTCACAAATAGAAAGATCTTTTGAAGATGAGAGGTT 404
 QY 497 IleGluTyrSerGlyLeu-----ThpGluThpGluLeuArgAlaIleThrGluLeuAla 514


```

QY      281 ProPromeProProsaengInProInThrThSerValLeuLeaIrgLysTyrAlaIle 300
        ||||| |||||::: |||||::: ||||| |||
Db      198 CCACACCTCTCTCTCTGACCAACAAC-----GTGATTCACAAAGAGACTGGC 148
QY      301 GtYAsPTrSerLysLeuLeuGluGlyAlaThrLeuGln----- 313
Db      147 TCACCTGAATTAACCTAAATAATMACCAAACTATCCAGAAATGCGAAGGAAATTGTTGAC 88
QY      314 -----LeuThrGtYAsPAsnValAsnSerPheGlnAla 324
        ||| |||||::: ||||| |||||
Db      87 TCTTCCTTTGTGTGAGACCTTTTAATGAAGTACAGGCA 49

RESULT 9
LOCUS   A2681177
DEFINITION ENTMR451R Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.
ACCESSION A2681177
VERSION  A2681177.1 GI:11818323
KEYWORDS GSS.
SOURCE   Entamoeba histolytica
ORGANISM Entamoeba histolytica
          Eukaryota; Entamoebidae; Entamoeba.
REFERENCE 1 (bases 1 to 863)
AUTHORS   Loftus,B., Van Aken,S. and Fraser,C.
          Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library
          Unpublished
JOURNAL   Contact: Brendan J Loftus
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 0208
          Fax: 301 838 3543
          Email: b.loftus@tigr.org
          Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library
          Seq primer: M13-Reverse
          Class: shotgun
          High quality sequence start: 16
          High quality sequence stop: 825.
FEATURES
     source
         1..863
            Location/Qualifiers
                /organism="Entamoeba histolytica"
                /mol_type="genomic DNA"
                /strain="HMI:IMSS"
                /db_xref="taxon:5759"
                /clone_lib="Entamoeba histolytica Sheared DNA"
                /note="Vector: PHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."
```

```

BASE COUNT      456 a      65 c      151 g      191 t
ORIGIN
Alignment Scores:
Pred. No.:      0.0942      Length:      863
Score:          114.50      Matches:      61
Percent Similarity: 43.41%  Conservative: 51
Best Local Similarity: 23.64% Mismatches: 103
Query Match:     2.90%      Indels:      43
DB:              28        Gaps:      12

US-09-494-297-2 (1-757) x A2681177 (1-863)
```

```

QY      479 LeuLysHisIleLysLysValIleGluLysGlyTyrArgGluLysGlyGlnAlaIleGlu 498
        |||::: |||||::: |||||::: |||||::: |||
Db      143 TTGAAGAAATTTAAAAAATGAGAAAATATTATAAGAGAAAGAAAGAAAG 202
QY      499 TyrSerGly-----LeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaIle 515
        |||
Db      203 AAAATTGAGAGAAAGAAATGTTAGAGAACTCAAAAAGAAATAGTACT--CAAAATAGAAA 259
QY      516 TyrTTrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPhe 535
        ::|||
Db      260 CATTATGACACACCTTGAAAAAGAAATTA---AAAGAAAAACCAAGAAATATC-----TTT 310
QY      536 GtYAsPMeLAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAsp 555
        |||::: |||
Db      311 GGGAAATTAAACCATCAAA---ATTGGAGTGGAAAAATTTATTATTAGAAAGTACGAAAGA 367
QY      556 SerAsnProProGlnLeuThrAspLeuAspPheIleProAsnAsnLysTyrGln 575
        |||
Db      368 ATAAATGAAGAAAGA-----CAATTTGAATGTT----- 397
QY      576 SerLeuIleGlyThrGlnTrpHisProGluAspLeuValAspIleIleArgMetGluAsp 595
        |||
Db      398 -----ACATTTCAACAGAAAGAAATGATGCTTAAGAGCAATTAATAAGAAAGA 448
QY      596 LysLysGluValIleProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLeu 615
        ::|||
Db      449 GAGAAAGAAAT-----AGTTCAACAGAAAAAATGCAATTTAGAAAAAAGAAATTTAT 496
QY      616 AlaGtYAsPArgThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGlu 635
        |||
Db      497 -----GATCTTAAGACAGAGATTCAACAAAGAAAT-----AATGAAAAAGAAAT 541
QY      636 LeuLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPheLysAspGlyLysAla 655
        ::|
Db      542 GAAATTAAACAAAGCTTGAAAGAAATATATACAGAAATGAATAAAGTGAAGAAATTA 601
QY      656 ThrIleAsnLeuLysHisGlyLysSerLeuThrLeuGlnGlyLeuProGluGlyTyrSer 675
        |||
Db      602 GCTAGTGTATTAGAAAGAAATGCAAAACTTAAATTAATGTTACATATAAGAAAGAA 661
QY      676 Tyr-----LeuValLysGluThrAspSerGluGlyTyrLysValLysVal 690
        |||
Db      662 TATGAGAAAGTGAATGAAATCTTATTAAACAAATCAAAAGAA----- 703
QY      691 AsnSerGlnGluValAlaAsnAlaThrValSerLysThrGlyValAspGlnLys 710
        |||
Db      704 -----CAAAAGTCATCCACAAAGTATGTAAGTAAATTCCAAGTTGAGTAACT 757
QY      711 LeuAlaPheGluAsnAsnLysGluProValIleProThrGlyValAspGlnLys 728
        ::|
Db      758 GTTCGAAAGTCTGATGATGACAAATTAATTAATTAAGACAAATGAAG 811

RESULT 10
LOCUS   BX350683/C
DEFINITION BX350683 Homo sapiens B CELLS (RAMOS CELL LINE) COR 25-NORMALIZED Homo sapiens cDNA clone CSOPL0081B09 3-PRIME, mRNA sequence.
ACCESSION BX350683
VERSION  BX350683.1 GI:30375505
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
          1 (bases 1 to 945)
          Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
          Full-length cDNA libraries and normalization.
          Unpublished
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: segr@genoscope.cns.fr, web : www.genoscope.cns.fr
```


Schein, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: <http://image.llnl.gov>
Series: IRAL Plate: 22 Row: 9 Column: 8
This clone has the following problem: frame shifted.

FEATURES

source

1.2421
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3050255"
/tissue_type="Skin, melanotic melanoma."
/clone_id="NIH-MGC_20"
/lab_host="DH10B-R"
/note="Vector: pOT87"

BASE COUNT 661 a 642 c 692 g 426 t
ORIGIN

Alignment Scores:

Pred. No.: 0.915 Length: 2421
Score: 112.00 Matches: 85
Percent Similarity: 33.41% Conservative: 52
Best Local Similarity: 20.73% Mismatches: 141
Query Match: 2.84% Indels: 132
Gaps: 20

US-09-494-297-2 (1-757) x BC008707 (1-2421)

QY 67 SerSerGluTyrArgTrpTyrGlyTyrGluSerTyrValArgGlyHisProTyrTyrLys 86
Db 849 AACGCCAGTTTACCTTTCGCGCTGCAGCAGTCTC-----AACCCCTACTATNAG 902
QY 87 GluPheArgValAlaHisAspLeuArgValAlaAsnLeuGluGlySerArgSerTyrGlnVal 106
Db 903 TTCATCCAGAACCCATGAA-----GAGGGA-----CGCTACACGTCTC 941
QY 107 TyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLysTrp 126
Db 942 CTGGCAGAAAC-----GAGGGA-----GAGGGA-----CGCTACACGTCTC 941
QY 127 TyrLysLysHisAspGlyLysSerThrLysPheGluAspTyrAlaMetSerProArgIle 146
Db 963 GAGAAAAAATCAGAGAGTCTGACATGAGAT-----GATGATGATGAGAA 1016
QY 147 ThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMetLysAsnGlyHisProGlnAsn 166
Db 1017 GATGGAAATTCATCCCTCTCTCTTGGC-----TCCAGAGAG 1058
QY 167 AlaAsnGlyLeuMetGluGluLeuGluProLeuAsnAlaIle----- 180
Db 1059 TGTAAACCGCTTAAGAGCTGATGAAAGCCCTTGAAGTACTGAGACCCAGATCATCCCTC 1118
QY 181 --ArgValThrGlnGlnAlaValAlaTyrTyrSerAspAsnAlaProIleSerAsnPro 199
Db 1119 GCAGCACTTGTCTGTAAGCAGAGCGTGCAGATTCCACCCCA-----CAACAAGCA 1175
QY 200 AspGluSerPheLysArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeu 219
Db 1176 GAGCGGTGGCGCTGAGCCCTCCAGAGTGAGTACACGACAGCTGACCGTGGCAGCC 1235
QY 220 MetArgGlnAlaLeuLysGlnLeuLysAlaAspProAsnLeuAlaThrLysMetProLysGln 239
Db 1236 ATGTATTACAGCTACTACATGCTACGCGAGCGACTTACTGCTGGCGCGCC----- 1289
QY 240 ValProAspAspPheGluLeuSerIlePheGluSerGluAspLysGlyAspLysTyrAsn 259
Db 1290 ---CTTCCCGGATTCATGCTACTTAC----- 1316
QY 260 LysGlyTyrGlnAsnLeuSerGly-----GlyLeuValPro 272
Db 1316

Db 1317 -----TACAGACACCTTCTCTGCTGGCGTGCAGCGTGTCTAATCCCTGGAGTGCAGACC 1370
QY 273 ThrLysProProThrProGly-----AspProProMetProProAsnGlnProGlnThr 291
Db 1371 ACCGCCACCACTCTCTGGAGCACACACACCGCCCAACACAGAGACTAGC 1430
QY 292 SerValLeuLeuArgLysTyrAlaIleGlyAspTyrSerLysLeuGluGlnGlyAlaThr 311
Db 1431 AGC-----GGGCCACCC 1442
QY 312 LeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAsp 331
Db 1442 ----- 1442
QY 332 IleGlyGluArgIleGluLeuSerAspGlyThrTyrThrLeuThrGluLeuAsnSerPro 351
Db 1443 -----TCCAAACCCACACCACTGACCTGGCCCC 1475
QY 352 AlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAlaGlyLysVal----- 369
Db 1476 GTGGCCGCATCATCCCGCCCGCCCGAGCTCAGCCGCTGATGACAGCTGGCCGAG 1535
QY 370 TyrThrIleLeuAspGlyLysGlnIleGluAsnProAsnLys----- 383
Db 1536 TATGTCCAGCAAGCGCTGAAGTTCAGACAGCAGTGTCTGTCACAAAGATGATCAAGA 1595
QY 384 ---GluLeuValGluProTyrSerValGluAlaTyrAsnAspPheGluGluPheSerVal 402
Db 1596 TTGAGTTCCTGAGCGGTG-----CACCACTATATATCTTATATGATTAAG-- 1646
QY 403 LeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGln 422
Db 1647 -----AAGCACTTCTCTCCAGAAAGAGGGCGCATACATGACAG 1688
QY 423 ValValTyrCysPheAsnAlaAspLeuLysSerProProAspSer----- 437
Db 1689 GCTGTG-----TCTGCACCAAGAGAGCTGCCACAGACTGTCTCCGAGAAAGCA 1739
QY 438 GluAspGlyLysThrMetThrProAsp 447
Db 1740 AGTATGCTGGAGAGTGGCGGCTGAA 1769
RESULT 12
BC015953 2430 bp mRNA linear HTC 24-OCT-2001
LOCUS Homo sapiens, similar to splicing factor, arginine/serine-rich 8
DEFINITION (suppressor-of-white-apricot, Drosophila homolog), clone
ACCESSION BC015953
VERSION BC015953.1 GI:16358985
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 2430)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (22-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
COMMENT Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DNP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadansystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 14 Row: 3 Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein
This clone has the following problem: frame shifted.

FEATURES

SOURCE

1..2430
location/qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3830054"
/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
/note="Vector: pORF7"

BASE COUNT 663 a 644 c 697 g 426 t

ORIGIN

Alignment Scores:

Pred. No: 0.921 Length: 2430
Score: 112.00 Matches: 85
Percent Similarity: 33.41% Conservative: 52
Best Local Similarity: 20.73% Mismatches: 141
Query Match: 2.84% Indels: 132
DB: 11 Gaps: 20

US-09-494-297-2 (1-757) x BC015953 (1-2430)

OY 67 SerSerGIuTYrAgtRPTyGlyTYrGluSerTYrValArgGlyHisProTYrTyrLys 86

DB 858 AACCCAGATTGACCTTCTGCGCTGACACACTACCTC-----AACCCCTACTATTAAG 911

OY 87 GluPheArgValAlaHisAspLeuArgValAsnLeuGluGlySerArgSerTYrGlnVal 106

DB 912 TTCATCCAGAAAGCCATGAA-----GAGGA-----CGCTACACGTGTC 950

OY 107 TYrCysPheAsnLeuLysAlaPheProLeuGlySerAspSerSerValLysLysTrp 126

DB 951 CTGCGAGAAAC-----AAAAAGTAC 971

OY 127 TYrLysLysHisAspGlyLysSerThyLysPheGluAspTYrAlaMetSerProArgLys 146

DB 972 GAGAAAAAATCAGAGAGTCAGCTGACATGAAGAT-----GATGATGATGAAGAA 1025

OY 147 ThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMetTYrAsnGlyHisProGlnAsn 166

DB 1026 GATGGGAAATTAACCTTCACTCCCTCTCTTGGC-----TCCAAAGAG 1067

OY 167 AlaAsnGlyLysMetGluGlyLeuGluProLeuAsnAlaLe-----180

DB 1068 TGTAAACCGCTTGAAGAGCTGATGAACCCCTTGAAGGTAGAGACCCAGATCATCCCTC 1127

OY 181 ---ArgAlaThrGlnGluAlaValTrpTYrSerAspAsnAlaProLysSerAsnPro 199

DB 1128 GCAGCACTTGTCTTAAGCAGCAGAGGTGACAGTTCCACTCCACCCCA---CACAGCGCA 1184

OY 200 AspGluSerPheLysArgGluSerAsnLeuValSerThySerGlnLeuSerLeu 219

DB 1185 GACGGTCGGCTGTGACAGCCCTCCAGAGTGAAGACGACGAGCTGACCGTGGCAGCC 1244

OY 220 MetArgGlnAlaLeuLysGlnLeuLysAspProAsnLeuAlaThrLysMetProLysGln 239

DB 1245 ATGATTATACAGCTACTACATGCTACGCGGACACTTACTGCGTGGCGCCGCC-----1298

OY 240 ValProAspAspPheGlnLeuSerIlePheGluSerGluAspLysGlyAspLysTYrAsn 259

DB 1299 ---CCTCCGGAATCGATGACTACTTAC-----1335

OY 260 LysGlyTYrGlnAsnLeuSerGly-----GlyLeuValPro 272

DB 1326 -----TACAGCACCTTCTCTGCTGGCTGACCGCTGTCTAATCCCTGAGTAGCAGACC 1379

OY 273 ThrLysProProThrProGly---AspProProMetProProAsnGlnProGlnThr 291

DB 1380 ACCGCCACCATCTCTGGGAGCAGACACACACCGCCGCCACACAGCAGACATAGC 1439

OY 292 SerValLeuIleArgLysTYrAlaIleGlyAspTYrSerLysLeuGluGlyAlaThr 311

DB 1440 AGC-----GGGCCACC 1451

OY 312 LeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAsp 331

DB 1451 -----1451

OY 332 IleGlyGluArgIleGluLeuSerAspGlyThyTrpThrLeuThrGlnLeuAsnSerPro 351

DB 1452 -----TCCACAACACACACACACCAAGTGCATGCTGCCCC 1484

OY 352 AlaGlyTYrSerIleAlaGluProIleThrPheLysValGluAlaGlyLysVal-----369

DB 1485 GTGGCCGCAATCATCCCCCGCCCGCAGCTCCAGCCCGCGATGACAACTGGCCGAG 1544

OY 370 TYrThrIleLeuAspGlyLysGlnIleGluAsnProAsnLys-----383

DB 1545 TATGTCGCGACAGACGCGCTGAGTGCAGACAGTGTCTGCCAAGATGATCAAGAA 1604

OY 384 ---GluIleValGluProTYrSerValGluAlaIleTYrAsnAspPheGluGluPheSerVal 402

DB 1605 TTTAGATTCCTGACGCGCTGG-----CACCAATATAATGCTTATATGAGTTAAG---1655

OY 403 LeuThrThrGlnAsnTYrAlaLysPheTYrAlaLysAsnLysAsnGlySerSerGln 422

DB 1656 -----AACCACTTCTCTCCAGAAAGAGGGCGATAGCATGACG 1697

OY 423 ValValTYrCysPheAsnAlaAspLeuLysSerProAspSer-----437

DB 1698 GCTGTG-----TTCGACCAAGAAAGGCTCCACAGACTGCTGCCGAGAGAGCA 1748

OY 438 GluAspGlyGlyLysThrMetThrProAsp 447

DB 1749 AGTGATGCTGGGAGATGCGCGCTGAA 1778

RESULT 13

LOCUS AK076636 1493 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched

library, clone:922502j23 product:similar to RSD-6 [fatius

norvegicus], full insert sequence.

ACCESSION AK076636

VERSION AK076636.1 GI:26345549

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

REFERENCE 2 Carninci,P. and Hayashizaki,Y.

Normalizaton and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL MEDLINE PUBMED 20499374 11042159

SHibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Kono,H., Akiyama,Y., Nishi,K., Kitanai,T., Tashiro,H., Itoh,M.,

Sunmi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

TITLE	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, S., Kawai, J., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
JOURNAL	RIKEN Integrated sequence analysis (RISA) system -384-format
PUBLISHED	Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE	20530913
AUTHORS	11076861
TITLE	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schiraldi, L.M., Staudil, F., Suzuki, R., Tomita, M., Wagner, U., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carinci, P., de Bonaudo, M.F., Brownstein, M.J., Bult, C., Fleischer, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamaya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzei, J., Mombarts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyszynski, B., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S., and Hayashizaki, Y.
JOURNAL	Functional annotation of a full-length mouse cDNA collection
PUBLISHED	Nature 409 (6821), 685-690 (2001)
REFERENCE	21085660
AUTHORS	11217851
TITLE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
JOURNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
PUBLISHED	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 1493)
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, I., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyu, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shilaki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp, fax: 81-45-503-9216)
COMMENT	cdna library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES	source
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493
FEATURES	/organism="Mus musculus"
FEATURES	/mol_type="mRNA"
FEATURES	/strain="C57BL/6J"
FEATURES	location/Qualifiers
FEATURES	1. 1493

OY	489	GLYIYRARGGLULYSGLYGLNAlAlleGluTYrSerGlyLeuThrGlnLeuArg	508
		: :	
Db	490	GGAGAAAAGAGTCGTACCCACTACTGAGTTCGTGGCACACTAGAG-----	537
OY	509	AlAlAlThrGlnLeuAlAlleTYrTYrPheThrSerAlAGluLeuAspLysAspLys	528
Db	538	-----GACAGTGGTGGC-----GAT	552
OY	529	LeuLysAspTYrHisGlyPheGlyAspMetAsnAspSerThrLeuAlAlAlAlLysIle	548
		:	
Db	553	GTGGAGGATGCGCTGTGATTTCCAGATGAAAGCACTGAAACT---GATGTTCTTCCTCT	609
OY	549	LeuValAlGluTYrAlAGlnAspSerAsnProGlnLeuThrAspLeuAspPheIle	568
Db	610	GCCACCTCAGATGCTCTGTAGTANGAGAGCTGTACAGGCACT-----GACTCCTTTAGT	663
OY	569	ProAsnAsnAlnLysTYrGlnSerLeuLeuGlyThrGlnTyrPHisProGluAspLeuVal	588
Db	664	CCTGAGGCTGGAGTCCCCCTCA-----ACTGAAAAGAGAGTACCACCACTTCCA	714
OY	589	AspIleIleArgMet---GluAspLysLysGluValIleProValThrHisAsnLeuThr	607
		: : :	
Db	715	GACATTAACCAATTGTCAGAGAGAGAAATGTAAGTATGATCAATGATGATTTTCAAGAAAT	774
OY	608	LeuArgLysThrValThrGlyLeuAlAGlyAspArgTYrLysAspPheHisPheGluIle	627
Db	775	AGGCCCAAAACTGTGACTAACTAAGTACTCCGAAAGAAAAAATTATACATGTTT	834
OY	628	GluLeu-----LysAsnAlnLysGlnGluLeuLeuSerGlnThr	640
Db	835	GAACTCACTAACTGGCGCTGAAAAGCCAAAGATTAATGTGAAGATCCTTTAAATCAGTAG	894
OY	641	ValLysThrAspLysThrAsp-----LeuGluPheLysAspGlyLysAlaThrIleAsn	658
Db	895	GAATCGACTGATGAGCTAAATGATTGATGAA-----AAGAAGACTCCAACT	942
OY	659	LeuLysHisGlyGluSerLeuThrLeuGlnGlyLeuProGluGlyTYrSerTYrLeuVal	678
		: : : :	
Db	943	GAGCAGAGTCCCATGCTGTCTGCTCACTGCTGCGAATCGAGGTATGACTTTATGTCT	1002
OY	679	-----LysGluThrAspSerGlnGlyTYrLysValLysValAsnSerGlnValAla	696
Db	1003	ACTGCTTCAGAACTGACACACGTCATGAGAGAAATCAGTATGAAACCAACCAAGATTGGCT	1062
OY	697	-----AsnAlaThrValSerLysThrGlyIleThrSerAsp	708
		:	
Db	1063	GAAAACGACACACAGACTCTGTCACTAATGTCAACAGAGAG	1104
RESULT 14			
LOCUS	AK077916	2167 bp	mRNA linear HTC 05-DEC-2002
DEFINITION		Mus musculus 13 days embryo male testis cDNA, RIKEN full-length	
		enriched library, clone:6030440B06 product:chaperonin subunit 6a	
		(zeta), full insert sequence.	
ACCESSION	AK077916		
VERSION	AK077916.1	GI:26097567	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	1 Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PubMed	10349636		
NUM	2		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
TITLE	Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to		
MEDLINE	prepare full-length cDNA libraries for rapid discovery of new genes		
NUM			

JOURNAL MEDLINE PUBMED AUTHORS	Genome Res. 10 (10), 1617-1630 (2000) 20499374 11042159 3
TITLE	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komoto,H., Akiyama,Y., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M., Sunii,N., Ishii,Y., Nakamura,S., Hazama,N., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasliwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
JOURNAL MEDLINE PUBMED AUTHORS	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multiplexed sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861 4
TITLE	Kawai,Y., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arikawa,T., Hara,A., Fukunishi,Y., Komoto,H., Adachi,J., Fukuda,S., Aizawa,K., Iwawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanka,I., Saito,T., Okazaki,Y., Gojodori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nkaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staudt,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barish,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fleischer,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hotmann,M., Hume,D.A., Kamlay,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Rling,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Wetz,C., Whitaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawai,H., Kohlski,S. and Hayashizaki,Y.
JOURNAL MEDLINE PUBMED AUTHORS	Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 21085660 11217851 5
TITLE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
JOURNAL MEDLINE PUBMED AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2167) Adachi,J., Aizawa,K., Akimura,T., Arikawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,M., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Hori,F., Imochani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Kondo,S., Komoto,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,K., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohmoto,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toy,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE JOURNAL	Direct Submission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.go.jp, URL: http://genome-gsc.riken.go.jp/ , Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.

REFERENCE 1 (bases 1 to 889)
 AUTHORS Lofthus, B., Wang, Z., Van Aken, S. and Fraser, C.
 TITLE Determination of clone end sequences from Entamoeba histolytica
 JOURNAL HMI: IMSS sheared DNA library (2001)
 COMMENT Unpublished
 Contact: Brendan J Lofthus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3343
 Email: b.lofthus@tigr.org
 Clones are derived from the Entamoeba histolytica HMI: IMSS sheared
 DNA library
 Seq primer: M13-Forward

Class: shotgun
 High quality sequence start: 18
 High quality sequence stop: 811.
 Location/Qualifiers
 1..889
 /organism="Entamoeba histolytica"
 /mol_type="genomic DNA"
 /strain="HMI:IMSS"
 /db_xref="taxon:5759"
 /clone_lib="Entamoeba histolytica sheared DNA"
 /note="Vector: pHOSt. Site 1: Bst I; Constructed at The
 Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA isolated from broth cultures of E. histolytica
 using a method described by Clark and Diamond (Clark,
 C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
 method for isolate identification. Exp. Parasitol.
 77:450.). The DNA was mechanically sheared to give a
 tight size distribution (~2 kb). The v + 1 method used for
 the library construction is described in detail in Smith,
 H.O. and Venter, J.C. (Making small insert libraries for
 whole genome shotgun sequencing projects. In Genome
 Sequencing: A Practical Approach, eds. M. Vaubin and B.
 Barrell, Oxford University Press, 1999)."

BASE COUNT 399 a 72 c 154 g 264 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.242 Length: 889
 Score: 111.00 Matches: 63
 Percent Similarity: 38.248 Conservative: 54
 Best Local Similarity: 20.598 Mismatches: 87
 Query Match: 2.818 Indels: 102
 DB: 28 Gaps: 15

US-09-494-297-2 (1-757) x BH132924 (1-889)

QY 467 ThrValLysProAlaGlyAspThrAspProAspThrPheLeuLysHisIleLysLysValIle 486
 DB 199 ACAATCAAGCAAGATGATATTAAACCA-----AAAAGGCTTGA 237
 QY 487 GluLysGlyTyrArgGluLysGlyLnaIleGluTyrSerGlyLeuThrGln 506
 DB 238 TTTAAA-----TTAGTTGAAGAAATAC 258
 QY 507 LeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLys 526
 DB 259 ATTAAGTACCACTGAAA-----GACGCAAGACAGATATATATT 297
 QY 527 AspLysLeuLysAspPtyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAla 546
 DB 298 GTGTCAATGAAGAAGATTATATC---TTGAAGAGATTATTGATAAA-----TGTAAG 345
 QY 547 LysIleLeuValGluTyrAlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPhe 566
 DB 346 AAATTATGTATTGATGAATGTCAAAATGTCAA----- 378
 QY 567 PheIleProAsnAsnLysTyrGlnSerLeuIleGlyThr----- 580

DB 379 TTCATATATCAACAAGATCAATTAAGCAAAATGAAATTAACAACCTGTAAATACCGAA 438
 QY 581 ---GlnTPRHisProGluAspLeuValAspIleIleArgMetGluAspLysLysGluVal 599
 DB 439 ATTAAGGAGAGCTTAGATTAATATTGAAAGCAATCATCACAAATGATTAATGAAGAATGTAAT 498
 QY 600 IleProValThrHisAsnLeuThrLeuAlaGlyLysThrValThrGlyLeuAlaGlyAspArg 619
 DB 499 ATTCAGAAACCAAGAAATATTATTAAAGAAAGATACAGAAAT----- 540
 QY 620 ThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuLeuSerGln 639
 DB 541 -----ATGAAATTAATTAATATACAAAAAAGATATA----- 570
 QY 640 ThrValLysThrAspLys-----ThrAsnLeuGlu 649
 DB 571 GAAATAGAAACAGATTAATTAAGAAATATTATTAAGAAATTTTCATGACGTATATTAA 630
 QY 650 PheLys---AspGlyLysAlaThrIleAsnLeuLysHisGlyGlySerLeuThrLeuGln 668
 DB 631 ATTAAGAGATATTATTAATGATGATGTTACAAATAGAAATGTCAGAAATTTATGTTTAT 690
 QY 669 GlyLeuProGluGlyTyrSerTyrLeuValLysGluThrAspSerGluGlyTyrLysVal 688
 DB 691 GGAGAGTTTGAACATTAT-----CGAATGTTCAA 720
 QY 688 LysValAsnSerGlnGluValAlaAsn-----AlaThrValSerLysThrGly 704
 DB 721 TTCATTAAATTGCAAGAACAGCTCAATATTGAATGTTGGATTGTAAATCATTTATTA 780
 QY 705 IleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGluProValValProThrGly 724
 DB 781 ATTACCACTGTCGAAGATTTGATTTTACTGTCATAGA-----ATTATAGG 828
 QY 725 ValAspGlnLysIleAsnGlyTyrLeuAlaLeuIleValIleAlaGlyLleSerLeuGly 744
 DB 829 TTATTAAAAAGGTTCACAGTTAT-----GTAGG 858
 QY 745 IleTPRGlyIleHisThr 750
 DB 859 TATTGGGTATTTCACACT 876

Search completed: August 19, 2003, 18:20:05
 Job time : 3365 secs

